

1/3

NH₂ — 1 — 2 — 3 — 4 — 5 —

200 6 257
VKDNKKNRKKPTPKPPVWDEAGSGLDNGDFKVTPDTSTQHNKVSTSPKITTAK MSF
KVTPDTSTQHNK

258 6 318
PINPRPSLPPNSDTSKETSLTVNKETTVETKETTTNKQTSFDGKEKTTSAKETQSIEKT

319 6 379
SAKDLAPTSKVLAKEPTPKAETTKGPALTPKEPASTTPKEPTPTTIKSAPTPKEPAPT

400 1050
TTKSAPTPKEPAPT.....(KEPAPT) 71.....PTPRKMTSTMPPELNPTSRIAEMLTTRPNO

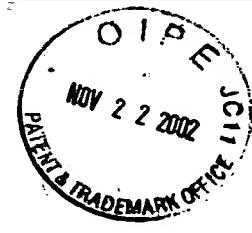
1082 6 1139
TPNSKLVEVNPKSEDAGGAEGEPTPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPML MSF
KSEDAGGAEGEPTPHMLLRPHVFMPEVTPDMDYLP

1141 7 1168 8
S-DETNICNGKPVDSLTLRNGTLVAFRG HYFWMLSPFSPPSPARRITEVWGIPSPI MSF
RG HYFWMLSPFSPPSPARRITEVWGIPSPI

1213 9
DTVFTRCNCEGKTFKK DSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAK MSF
KGFGGLTGQIVAALSTA
DTVFT

1263
YKNWPESVYFFK — 10 — 11 — 12 — COOH

Fig. 1



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v0 1 2 3 4 5 ...(KEPAPTT)₇₆... 7 8 9 10-12

v1 1 2 3 4 ...(KEPAPTT)₇₆... 7 8 9 10-12

v2 1 2 3 ...(KEPAPTT)₇₆... 7 8 9 10-12

v3 1 3 ...(KEPAPTT)₇₆... 7 8 9 10-12

2 3 SOMATOMEDIN B-LIKE DOMAIN
4 5 HEPARIN SULFATE BINDING DOMAIN
(KEPAPTT)₇₁ EXON 6 BOUNDARY LUBRICATION DOMAIN
8 9 HEMOPEXIN-LIKE REPEATS

Fig. 2A

ISOFORM	ARTICULAR CHONDROCYTES			SYNOVIAL FIBROBLASTS			PREDICTED MOLECULAR WEIGHT
	EXON 2	EXON 4	EXON 5	EXON 2	EXON 4	EXON 5	
V0	+	+	+	+	+	+	151.096 kDa
V1	+	+	-	+	+	-	146.327 kDa
V2	+	-	-	+	-	-	140.894 kDa
V3	-	-	-	-	-	-	135.207 kDa

Fig. 2B

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502 630
V1 ATA ACA GAA [GAA....AAA] GTA AAA GAT AAC

exon 4 exon 5 exon 6
I¹⁵⁴ T¹⁵⁵ E¹⁵⁶ V²⁰⁰ K D N²⁰³

352 630
V2 GAG AGT TTC TGT GCA GAA [GTG....AAA] GTA AAA GAT AAC

exon 3 exon 4 exon 6
E¹⁰¹ S F C¹⁰⁴ A¹⁰⁵ E¹⁰⁶ V²⁰⁰ K D N²⁰³

109 352 630
V3 TCA TCT CAA [GAT....GCG] GAG....TGT GCA GAA [GTG....AAA] GTA AAA GAT AAC

exon 1 exon 2 exon 3 exon 4 exon 6
S²³ S²⁴ Q²⁵ E^{67....104} A¹⁰⁵ E¹⁰⁶ V²⁰⁰ K D N²⁰³

Fig. 3